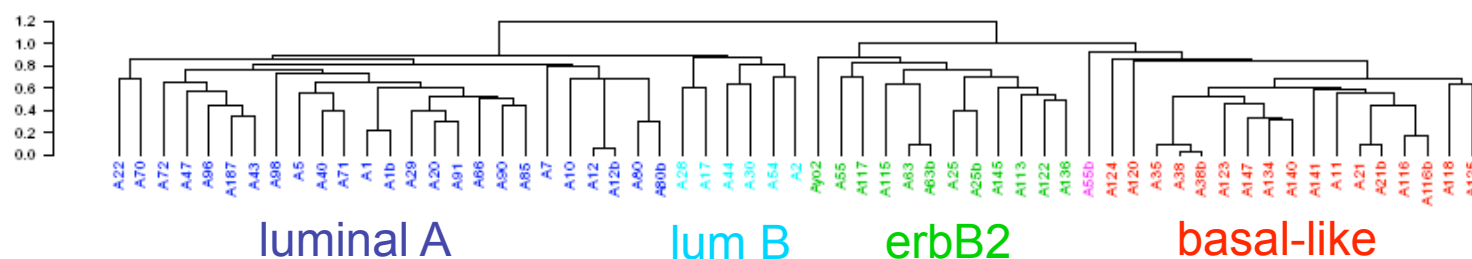


**Supplemental Figure 1:** Hierarchical clustering of 61 reference tumor samples using “intrinsic genes” of Sørli et. al. (PNAS 2001 98(19): 10869-74).



**Supplemental Figure 1:** Sample dendrogram of gene expression hierarchical cluster analysis of a reference tumor cohort with the “intrinsic genes” (Sørli, et. al. PNAS, 2001). The height of the dendrogram branches (scale on left) indicate degree of similarity with neighboring samples (shorter branches are more similar). Sample names of 61 primary tumor samples are indicated below the dendrogram; sample replicates are indicated by sample names ending with “b”. Intrinsic subtype of each cluster was determined by correlation of cluster centroids to the original centroids of Sørli et. al, and are color coded as follows: luminal A in blue, luminal B in teal, erbB2 in green, and basal-like in red.

**Supplemental Figure 2:** Correlation of BRCA1 expression level measured by qRT-PCR between exon1 and exon 2 and BRCA1 promoter methylation

